Table 1

S. aureus - Coding regions containing known sequences

+ Contig ID	+ O H	ta nt	i ŭ i	-+		percent ident	HSP nt length	
	 	41	1 757		S.aureus DNA for hld gene and for part of agr gene	1000 1		663
 	2	3273		emb X52543 SAAG	S.aureus agrA, agrB and hld genes	1 66 1	1 608	I (VI -
	- 5	i 47 i	9	dbj D14711 STAH	Staphylococcus aureus HSP10 and HSP60 genes		223	9
	- - - -	07	l m	emb X72700 SAPV	S.aureus genes for S and F components of Panton-Valentine leucocidins	81	216	369
	4 - 4			emb X72700 SAPV	alentine leucocid	95 1		أفأنا
10	 	1 00	. •	gb L25288	(Staphylococcus aureus gyrase-like protein alpha and beta subunit (grlA and grlB) genes, complete cds	86	715	819
16	 	1 5302	6246	gb U35773	Staphylococcus aureus prolipoprotein diacylglyceryl transferase (lgt) gene, complete cds	94	251	945
16	9	6249	7091	gb U35773	Staphylococcus aureus prolipoprotein diacylglyceryl transferase (lgt) gene,	66	843	843
16		7084	7584	gb U35773	Staphylococcus aureus prolipoprotein diacylglyceryl transferase (lgt) gene,	66	342	501
50	 	995	1 549	gb L19300	Staphylococcus aureus DNA sequence encoding three ORFs, complete cds; prophage phi-11 sequence homology, 5' flank	100	443	447
50	7	1011	841	gb L19300	Staphylococcus aureus DNA sequence encoding three ORFs, complete cds; prophage phi-11 sequence homology, 5' flank	91	137	171
50	m 		1798	gb L19300	Staphylococcus aureus DNA sequence encoding three ORFs, complete cds; prophage phi-11 sequence homology, 5' flank	100	110	213
	4 -	1 5300	1 3825	gb M76714	Staphylococcus aureus peptidoglycan hydrolase gene, complete cds	100	948	1476
	ر ب	├	2 1	gb M76714	ne, complete c		309	507
				gb U41072	Staphylococcus aureus isoleucyl-tRNA synthetase (iles) gene, partial cds		126	144
	7	00 1	ויטו	gb U41072	Staphylococcus aureus isoleucyl-tRNA synthetase (ileS) gene, partial cds	_	430	474
1 26	ر ا		53	emb X74219 SAIL	aureus gene for isoleucyl-tRNA synthetase			2769
	-	_	1 4392		Staphylococcus aureus DNA fragment with class II promoter activity		⊢ ⊢ I	3132
	114	4	113463	emb X73889 SAP1	S.aureus genes Pl and P2	66		1515
		4	38		S.aureus genes Pl and P2		\sim 1	
38		42	113112		S.aureus geh gene encoding lipase (glycerol ester hydrolase)			1173
38	119		LO I	gb M12715	S.aureus geh gene encoding lipase (glycerol ester hydrolase)		2085	2085

Table 1

S. aureus - Coding regions containing known sequences

Contig	10RF	Start (nt)	Stop (nt)	-+	+	percent ident	HSP nt length	ORF nt
46	2	519	1727	gb U73374 	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8E, cap8E, cap8C, cap8D, cap8E, cap8E, cap8E, cap8K, cap8E, cap8K, cap8E, cap8K, cap8E, cap8N, cap8N, cap8O, cap8P, complete cds	+	1209	1209
46	+	1720	2295	gb U73374	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8D, cap8E, cap8F, cap8K, cap8	8 6	576	576
4	4	2259	3182	gb U73374	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8F, cap8N, cap8N, cap8N, cap8N, cap8N, cap8N, cap8N, cap8O, cap8P, complete cds	97	924	924
46		3173	ı ص	gb U73374	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8K, cap8	86	1283	1326
46	9	4536 1 4536 1	5720	gb U73374	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8D, cap8E, cap8F, cap8K, cap8	866	:	1185
46	·	6455 6455 	6120	gb U73374	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8D, cap8E, cap8F, cap8F, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	66	278	336
48	. — - ! !	2	l RJ	dp L25893	Staphylococcus aureus recA gene, complete cds	66	954	954 +
	m	1 4465	1 2924	emb x85029 sAAH	S.aureus AhpC gene	100	88	1542
1 50	4	ا 🛁 ا	51		- 2	1 86 1	540	594
1 54	т К	0	39		S.aureus fnbB gene for fibronectin binding protein B	100	1668	1683
1 54	7 1	1 4865	2	emb X62992 SAFN	S.aureus fnbB gene for fibronectin binding protein B		720	744
1 54	S	Öi	∵oʻi		S.aureus fnbB gene for fibronectin binding protein B	100	463	495
	9	നി	30		S.aureus fibronectin-binding protein (fnbA) mRNA, complete cds	100	3087	3087
28	- π ! - π !	-	 			68	89	1077
28	7 7	1 2858	28		S.aureus abcA, pbp4, and tagD genes	1 66 1	423	423
28			70		S.aureus abcA, pbp4, and tagD genes	1 66 1	1305	1305
28	9	5677	5378	gb U29478	Staphylococcus aureus ABC transporter-like protein AbcA (abcA) gene, partial cds	100	300	300
200	7	9805		lemb X91786 SAPB	S.aureus abcA, pbp4, and tagD genes	1 66 1	1755	1755
					S.aureus agr gene encoding an accessory gene regulator protein, complete cds	100		444
1 72	5 -	1 2457	1 1453	emb X52543 SAAG	S.aureus agrA, agrB and hld genes	1 66 1	673	1005

Table

S. aureus - Coding regions containing known sequences

	g t	3561	3651	324	477	204	174	705	1 4 7 7	1920	1128	1125	2652	258	450	516	681
+	r ng	2396	3171	320	477	154	164	705	1 477	1920	1128	1125	099	1 89	450	516	61
+	ident	66	- 66	100	100	1001	+ — — 	94	66	8 6	97	97	83	1 6	100	66	100
+	ה אם וום הוא הוא הוא הוא הוא הוא הוא הוא הוא הוא	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	S.aureus DNA for rpoC gene	aphylococcus aureus ribosomal protein S12 (r) ibosomal protein S7 (rpsG) and ORF 1 genes,	Staphylococcus aureus ribosomal protein S12 (rpsL) gene, complete cds, ribosomal protein S7 (rpsG) and ORF 1 genes, partial cds	Staphylococcus aureus ribosomal protein S12 (rpsL) gene, complete cds, ribosomal protein S7 (rpsG) and ORF 1 genes, partial cds	phylococ p8E, cap	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8K, cap8	aphylococcus aureus tyjap8E, cap8E, cap8F, complete	phylococcus aureus type 8 capsule genes, c p8E, cap8F, cap8G, cap8H, cap8I, cap8J, ca p8O, cap8P, complete cds	aphylococcus aureus ty ap8E, cap8F, cap8G, ca ap8O, cap8P, complete	phylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8E, cap	S.aureus gene for clumping factor	Staphylococcus aureus isoleucyl-tRNA synthetase (ileS) gene, partial cds	Staphylococcus aureus ORF1, partial cds, ORF2, ORF3, autolysin (atl) genes, complete cds	Staphylococcus aureus ORF1, partial cds, ORF2, ORF3, autolysin (atl) genes, complete cds	Staphylococcus aureus prolipoprotein signal peptidase (lsp) gene, complete cds
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	acession	emb X64172 SARP	emb x89233 sARP	gb U20869	gb U20869	gb U20869	gb U73374 	gb U73374	gb U73374	gb U73374 	gb U73374	gb U73374	emb 218852 SACF	gb U41072	gb L41499	gb L41499 	gb M83994
	(nt)	3917	7677	8908	8579	8821	191	E တ ဆ	1660	3503	4521	5643	ıω	882	452	1041	1958
1 1 1 1 1 N	(nt)		4027	7745	8103	8618	18	1 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8	887	1584	3394	4519	1 (2)	625	ו מי	ιQ	1278
++	OIL		2	+ ·		5	+ - ·	5	m 	4	S	9	2 -	2 -	·	7	2 -
	ID		82	85	82	82	8 7	80	89	84	84	84	96	6	111	111	117

Table

S. aureus - Coding regions containing known sequences

	† - - -	 	 	1		+		++
ontig ID	ORF	ta nt	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
Ι ω	7	3787	4254	dbj D30690 STAN	Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete cds	6 6 6	467	468
30	+		3640	emb X13290 SATN	Staphylococcus aureus multi-resistance plasmid pSK1 DNA containing transposon Tn4003	78	956	1044
30	+ — -		4265	emb z16422 SADI	S.aureus dfrB gene for dihydrofolate reductase	86	416	453
	+ - 9	l CO	1 ~	emb 216422 SADI	S.aureus dfrB gene for dihydrofolate reductase	1 86	607	864
	+ 5	29	20	emb X71437 SAGY	S.aureus genes gyrB, gyrA and recF (partial)	97	838	912
36	++	111680	1 8	dbj D10489 STAG	Staphylococcus aureus genes for DNA gyrase A and B, complete cds	100	2694	2694
36	- 9 -	i co	110940		A gyrase A and	1 66	1947	1947
	+	iΩ	111765	gb 877055	recF cluster: dnaA=replisome assembly proteingyrB=DNA gyrase beta subunit [Staphylococcus aureus, YB886, Genomic, 5 genes, 3573 nt]	66	822	828
			1 2867	1628981961	Staphylococcus aureus S-adenosylmethionine synthetase gene, complete cds	1 66	1305	1305
43		10	1 4281	gb L42943	Staphylococcus aureus (clone KIN50) phosphoenolpyruvate carboxykinase (pckA) gene, complete cds	100	1170	1182
43		4254	4718	gb U51133	Staphylococcus aureus phosphoenolpyruvate carboxykinase (pcka) gene, complete cds	100	449	465
43	б	7269 1	1 7261	gb U51132	Staphylococcus aureus o-succinylbenzoic acid CoA ligase (mene), and o-	100	75	285
43	100	9464	8361	gb U51132	Staphylococcus aureus o-succinylbenzoic acid CoA ligase (mene), and o-	100	1104	1104
43		111232	9748	gb U51132		100	1485	1485
43	112	110739	110320	gb U51132	Staphylococcus aureus o-succinylbenzoic acid CoA ligase (mene), and o-	100	332	420
52	2	2454	3437	emb X58434 SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	1 66	305	984
225	9	3513	4820	emb X58434 SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	86	1308	1308
52	7	4818		emb X58434 SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	66	1413	1413
53	-	387	1526	gb s77055	recF cluster: dnaA=replisome assembly proteingyrB=DNA gyrase beta subunit [Staphylococcus aureus, YB886, Genomic, 5 genes, 3573 nt]	66	1140	1140
1 2 2 3	2	1877	2152	gb S77055	recF cluster: dnaA=replisome assembly proteingyrB=DNA gyrase beta subunit [Staphylococcus aureus, YB886, Genomic, 5 genes, 3573 nt]	100	276	276
						-		

Table 1

S. aureus - Coding regions containing known sequences

Contig	ORF	ta nt	Stop (nt)	match acession	match gene name	percent	HSP nt Length	ORF nt
153	 m 	214	28 1	gb s77055	recF cluster: dnaA=replisome assembly proteingyrB=DNA gyrase beta subunit [Staphylococcus aureus, YB886, Genomic, 5 genes, 3573 nt]	66	113	147
		079		gb U06451	Staphylococcus aureus proline permease homolog (putP) gene, complete cds	91	154	1479
154	111	1 9935	9615	gb U06451	Staphylococcus aureus proline permease homolog (putP) gene, complete cds	1 66 1	229	321
		994	16	gb U06451	Staphylococcus aureus proline permease homolog (putP) gene, complete cds		12	225
1 154		08	50	gb U06451	Staphylococcus aureus proline permease homolog (putP) gene, complete cds		1326	1413
	5			dbj D28879 STAP	Staphylococcus aureus gene for penicillin-binding protein 1, complete cds	1000	71	984
ب ب	m — —		1 😽 🗆	_	Staphylococcus aureus prolipoprotein signal peptidase (lsp) gene, complete cds	92	203	327
1 162		1406	1 705	gb U21221	Staphylococcus aureus hyaluronate lyase (hysA) gene, complete cds	100	702	702
199	4			gb U19770 	Staphylococcus aureus pyrrolidone carboxyl peptidase (pcp) gene, complete cds	96	127	510
164	7 -	4774		dbj D86727 D867	Staphylococcus aureus DNA for DNA polymerase III, complete cds	66	3470	4344
168		1 7448	6447	gb U21636	Staphylococcus aureus cmp-binding-factor 1 (cbf1) and ORF X genes, complete cds	100	1002	1002
168	ω 		1 7961	gb U21636	Staphylococcus aureus cmp-binding-factor 1 (cbf1) and ORF X genes, complete cds	66	1158	1578
1 173	9	24		gb J03479‡	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-	100	1440	1440
173		111252	9522	gb J03479	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta- galactosidase (lacG) genes, complete cds	66	1731	1731
ı <u>r</u> -	80	8285	8704	gb J034791	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta- galactosidase (lacG) genes, complete cds	100	420	420
173	o	10168	6836	gb J03479	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta- galactosidase (lacG) genes, complete cds	100	330	330
ı [~	110	111815	110829	emb X14827 SALA	Staphylococcus aureus lacC and lacD genes	100	987	1 286
1 173		27 27 	i 귺 i	emb X14827 SALA	Staphylococcus aureus lacC and lacD genes	100	948	948
	112	283	230	gb M64724	S.aureus tagatose 6-phosphate isomerase gene, complete cds	100	534	534
7	113			gb M32103	Staphylococcus aureus lac repressor (lacR) gene, complete cds and lacA repressor (lacA), partial cds	100	471	471
173	114	114633	113866	gb M32103	Staphylococcus aureus lac repressor (lacR) gene, complete cds and lacA repressor (lacA), partial cds	100	768	768
.	+-	 			, 	+	i 	<u>+</u>

Table

S. aureus - Coding regions containing known sequences

+	654	720	453	303	765	270	525	339	1623	1611	822	1920	177	1203	870	324	306	1143	873	1557	1 708 1	342
HSP nt length	115	720	453	303	765	270	499	277	1332	119	132	1920	177	250	870	324	304	1143	444	1552	684	157
	100	100	100	100	66	1 66	66	86	97	66	06	66	66		66	66	97	-	94	66	66	96
+		Staphylococcus aureus holin-like protein LrgA (lrgA) and LrgB (lrgB) genes,	Staphylococcus aureus holin-like protein LrgA (lrgA) and LrgB (lrgB) genes,	Staphylococcus aureus holin-like protein LrgA (lrgA) and LrgB (lrgB) genes, complete cds	Staphylococcus aureus lytS and lytR genes, complete cds	Staphylococcus aureus lytS and lytR genes, complete cds	S.aureus sigma factor (plaC) gene, complete cds	Staphylococcus aureus spa gene for protein A	S.aureus spa gene coding for protein A, complete csd	Staphylococcus aureus spa gene for protein A	(Staphylococcus aureus chorismate synthase (aroC) and nucleoside diphosphate kinase (ndk) genes, complete cds, dehydroauinate synthase (aroB) and geranylgeranyl pyrophosphate synthetase homolog (gerCC) genes, partial cds	a gene for coagulase	Staphylococcus aureus gene for staphylocoagulase		Staphylococcus aureus lysyl-tRNA sythetase gene, complete cds, transfer RNA (tRNA) genes, 5S ribosomal RNA (5S rRNA) gene, 16S ribosomal RNA (16S rRNA) gene, 23S ribosomal RNA (23S rRNA) gene	S.aureus ptsH and ptsI genes	S.aureus ptsH and ptsI genes	S.aureus orfs 1,2,3 & 4	S.aureus genes Pl and P2	Staphylococcus aureus atl gene for autolysin, complete cds and other ORFs	Staphylococcus aureus ORF1, partial cds, ORF2, ORF3, autolysin (at1) genes, complete cds	Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB, dltC and dltD genes, complete cds
+	gb U52961	gb U52961	gb U52961	gb U52961	gb L42945	gb L42945	dp M63177	emb(X61307 SASP	gb J01786	emb X61307 SASP	gb U319791	emb X17679 SACO	emb X16457 SAST	emb X16457 SAST	gb L36472	emb x93205 sAPT		emb(X97985 SA12	emb(X73889(SAP1	dbj D17366 STAA	gb L41499	dbj D86240 D862
Stop (nt)	655	1482	1909	ico	I 1	3025	1 0	341	l W	25	1 0	I ~	1 4	5	872	01	31	30	2175	5.5	23	7770
Start (nt)	2	2201	2361	55.	i	I O	ı ⊣	i m	1 0	1 00		1 4	96	5768	74	68	10	63	1303	-	2939	7429
† – –	† — — ·	2	m 	- 4	+ - ·	9	 	+ — ·			! ! ↔ ! → → - ·	 			 		4		- 5		2 - 2	
+ Contig ID	178	178	178	178		1 ~	1 181	Ιœ	1 182	ıœ	1 00		ı ه	1 191	l O	ıσ	10	0	1 202	. ←	—	214

Table 1

S. aureus - Coding regions containing known sequences

Contig	++ ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent jdent	HSP nt langth	ORF nt
I —	+ 8		:	emb X72700 SAPV	S.aureus genes for S and F components of Panton-Valentine leucocidins	+ 4 1 1 1 0 0 1 0	265	921
219	2	1810	1073	dbj D30690 STAN	Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete cds	100	09	738
219	 	2979	2035	dbj D30690 STAN	Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete cds	66	945	945
219	+ ·	4359	+ 3196 	dbj D30690 STAN	Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete cds	+	1164	1164
219	·	7044	5176	dbj D30690 STAN	Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete cds	+ — — - 1 86 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1869	1869
219	9	6557	5883	dbj D30690 STAN	Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete cds	+ — — - - - - - - - - - - - - - -	675	675
219		6801	6334	dbj D30690 STAN	Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete cds	86	468	468
221	+	10816	110034	gb L19298 	Staphylococcus aures phosphatidylinositol-specific phospholipase C (plc) gene, complete cds	91	1	783
223		2855	1506	gb U73374	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8K, cap8	66	102	1350
		2	1357	emb x97985 SA12	S.aureus orfs 1,2,3 & 4	100	176	1356
1 234			1 2485	emb x97985 sA12	S.aureus orfs 1,2,3 & 4		6	792
I M I	3	2648	3148	emb x97985 SA12	S.aureus orfs 1,2,3 & 4	_	0 1	0
	6 1			emb(x97985 SA12	S.aureus orfs 1,2,3 & 4		1305	ထြား
M	9 1	00	ന്	gb U488261	Staphylococcus aureus elastin binding protein (ebpS) gene, complete cds			
4		2	0	emb X62288 SAPE		0 1	103	402
ו עד ו	2	ι <u>α</u> ο Ι		gb L25426	Staphylococcus aureus penicillin-binding protein 2 (pbp2) gene, complete cds	66	465	
I SO I	1 2	1539	1 1093	gb U465411	Staphylococcus aureus sarA gene, complete cds	1 96	447	447
	1 2	ו גא ו	1835	gb U57060	Staphylococcus aureus scdA gene, complete cds	94	142	
	3		2	dp 057060	Staphylococcus aureus scdA gene, complete cds	1 66 1	756	756
9		2	6	dp M90693	Staphylococcus aureus glycerol ester hydrolase (lip) gene, complete cds		1213	1899
265	; ; ; ;	н	7 1	dbj D21131 STAS	Staphylococcus aureus gene for a participant in homogeneous expression of high-level methicillin resistance, complete cds	- 66	941	942

Table 1

S. aureus - Coding regions containing known sequences

iξH	ORF	Start (nt)	Stop (nt)	match acession	match gene name	percent	HSP nt length	ORF nt length
265		889	476	dbj D21131 STAS	Staphylococcus aureus gene for a participant in homogeneous expression of high-level methicillin resistance, complete cds	66	213	213
i 90	. e	2418	1 1765	dbj D21131 STAS 	Staphylococcus aureus gene for a participant in homogeneous expression of high-level methicillin resistance, complete cds	86	69	654
266		2		dbj D14711 STAH	Staphylococcus aureus HSP10 and HSP60 genes	1 86	743	1017
282	·		1 525	gb S72488	hemB=porphobilinogen synthase [Staphylococcus aureus, SA1959, Genomic, 1087 nt]	100	110	525
1 282	2	516	1502	gb S72488	hemB=porphobilinogen synthase [Staphylococcus aureus, SA1959, Genomic, 1087 nt]	100	952	987
284	 	e -	170	gb M63176 	Staphylococcus aureus helicase required for T181 replication (pcrA) gene,	86	84	168
284	8	1 282	1034	gb M63176	Staphylococcus aureus helicase required for T181 replication (pcrA) gene,	100	712	753
284		1028	1 2026	gb M63176 	Staphylococcus aureus helicase required for T181 replication (pcrA) gene, complete cds	66	979	666
284	+	1990	1 2202	gb M63176	Staphylococcus aureus helicase required for T181 replication (pcrA) gene,	86	187	213
289	8	1536	1991	gb M32470	S.aureus Sau3AI-restriction-enzyme and Sau3AI-modification-enzyme genes, complete cds	66	338	456
			8 9 8	gb L01055 	Staphylococcus aureus gamma-hemolysin components A, B and C (hlgA, hlgB, hglC) genes, complete cds	66	867	867
0	5	1409	2383	gb L01055 	Staphylococcus aureus gamma-hemolysin components A, B and C (hlgA, hlgB, hglC) genes, complete cds	100	975	975
303	ε Ε	2367	3161	gb L01055 	Staphylococcus aureus gamma-hemolysin components A, B and C (hlgA, hlgB, hglC) genes, complete cds	66	793	795
0		2707	1355	dbj D17366 STAA	Staphylococcus aureus atl gene for autolysin, complete cds and other ORFs	66	1343	1353
311	- -	1 2628	M	gb L42945	ا تِنَا	86	1314	<u>ب</u> ز
-	9 -	7019	<u>ر</u> ا	gb L14017	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	74	351	852
i (2) i		1998	1003	gb U31175 	Staphylococcus aureus D-specific D-2-hydroxyacid dehydrogenase (ddh) gene, complete cds	86	966	966
1 2			. ന I	lemb Y00356 SASP	Staphylococcus aureus V8 serine protease gene	100	108	237
1 338	- +		388	emb X64389 SALE	S.aureus leuF-P83 gene for F component of leucocidin R	86 -	259	300
നി	5	1828	0	emb X64389 SALE	S.aureus leuF-P83 gene for F component of leucocidin R		137	741

Table 1

S. aureus - Coding regions containing known sequences

ORE nt length			2	501	537	672	903	405	1146	657			762	216	216	1248	324	432	708	807	168	657
HSP nt length	1176		F 1	ω 1	537	671	42	89	1146	349			163	216		1248	200	432	151	556	134	657
percent ident	100	86	96	100	66	75	86	97	66	97			66	100	100	66	96	100	100	100	100	97
match gene name	Staphylococcus aureus SA4 Fts2 (fts2) gene, complete cds	S.aureus mRNA for nuclease	S.aureus bacteriophage phi-11 attachment site (attB)	Staphylococcus aureus prolipoprotein signal peptidase (lsp) gene, complete cds	Staphylococcus aureus prolipoprotein signal peptidase (lsp) gene, complete cds	Staphylococcus aureus MHC class II analog gene, complete cds	Staphylococcus aures phosphatidylinositol-specific phospholipase C (plc) gene, complete cds	Staphylococcus aures phosphatidylinositol-specific phospholipase C (plc) gene, complete cds	S.aureus DNA for penicillin-binding protein 2	S.aureus target site DNA for IS431 insertion	S.aureus hlb gene encoding sphingomyelinase	Staphylococcus aureus hlb gene for beta-hemolysin	asp23=alkaline shock protein 23 {methicillin resistant} [Staphylococcus aureus, 912, Genomic, 1360 nt]	Staphylococcus aureus ORF1, partial cds, ORF2, ORF3, autolysin (atl) genes, complete cds	Staphylococcus aureus atl gene for autolysin, complete cds and other ORFs	1 and IS1182 (fro	S.aureus (strain RN450) transposon Tn554 insertion site	Staphylococcus aureus gene for penicillin-binding protein 1, complete cds	ing prote	Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB,	Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB, dltC and dltD genes, complete cds	S.aureus factor essential for expression of methicillin resistance (femA) gene, complete cds, and trpA gene, 3' end
match acession	gb U06462	emb v01281 SANU	dp M20393	gb M83994	gb M83994 gb M83994	dp 10202031	gb L19298	gb L19298 	emb X62288 SAPE	emb X62282 SATS	emb X61716 SAHL	emb X13404 SAHL	gb S76213	gb L41499 	dbj D17366 STAA	gb L43098	gb K02985	dbj D28879 STAP	dbj D28879 STAP	dbj D86240 D862	dbj D86240 D862	emb X17688 SAFE
	1754	1 2	230	I		1 1		1507	1148	1248	I 4		i 0	. ←	639	ıν	1 325		I ~	808	1 0	685
Start (nt)	7.9	ı	l n	01	1582			1103		1904	1	69		7	l D		Í	9	1829	2 1	832	1341
‡ 2 H .	2	2	·	· · · · · · · · · · · · · · · · ·	2	+ — ·		~ ~ ·	. — · ! !		, — . 	1 2		·	2	N	 	; - - - - -	7	 	7	
+ Contig ID	1 4	1 4	4	i LO	l ß	356	ıφ	9	l [~	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	0	1 0	i 0	418	1	i∼v	I (V		427	l CO		436

Table 1

S. aureus - Coding regions containing known sequences

Start Stop match match gene name (nt) (nt) acession	+		ch gene n		percent	HSP nt length	+ ORF nt (length (
++- 03 1657 6 	557 6	. Ψ	emb X17688 SAFE	S.aureus factor essential for expression of methicillin resistance (femA) gene, complete cds, and trpA gene, 3' end	100	294	747
1300 emb	emp	1 — 1	X72700 SAPV	S.aureus genes for S and F components of Panton-Valentine leucocidins	84	204	954
6 2	78	gb [1	1010551	Staphylococcus aureus gamma-hemolysin components A, B and C (hlgA, hlgB, hglC) genes, complete cds	86	187	273
67 1078 gb	α 6 - 8	Ω	U197701	Staphylococcus aureus pyrrolidone carboxyl peptidase (pcp) gene, complete cds	100	51	912
76 1784 gb	4 1 gb	i q	10776101	Staphylococcus aureus pyrrolidone carboxyl peptidase (pcp) gene, complete cds	96	597	609
9 4319	- 6	e e	emb Z18852 SACF	S.aureus gene for clumping factor	75	653	2991
	-+ 91 67 1	i g	11252881	Staphylococcus aureus gyrase-like protein alpha and beta subunit (grlA and grlB) genes, complete cds	66	2418	2418
20 6792 gb	92	i g	L25288	Staphylococcus aureus gyrase-like protein alpha and beta subunit (grlA and grlB) genes, complete cds	66	1328	1329
99 en	1 6 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ë	emb X52543 SAAG	S.aureus agrA, agrB and hld genes	100	76	324
22 1560 6	09	6	emb X64172 SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	100	250	363
44 1534 em	34	i iii	emb X64172 SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	1000	224	291
388 1188 g¤	61 88	αβ	P W83994	Staphylococcus aureus prolipoprotein signal peptidase (lsp) gene, complete cds	86	72	201
2737 1370 gb	1 0/	5	0 021221	Staphylococcus aureus hyaluronate lyase (hysA) gene, complete cds	1 66	1368	1368
ι S	e	η _g i	M83994	pti	100	108	483
613 2242 gb	42 g	de l	L14017	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	84	323	630
2 2700 9	61 00	gr	b S76213	asp23=alkaline shock protein 23 (methicillin resistant) (Staphylococcus aureus, 912, Genomic, 1360 nt]	96	423	423
1297	97	9 I	emb X72014 SAFI	S.aureus fib gene for fibrinogen-binding protein	66	540	540
6 1801	01 -	i & i	emb X72013 SAFI		1 66	221	Θi
1 1092	92	븅	dbj D17366 STAA	Staphylococcus aureus atl gene for autolysin, complete cds and other ORFs	66	641	1059
 		1				• 	•

Table 1

S. aureus - Coding regions containing known sequences

Contig (C	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt
+ -		58	963	gb L19300	Staphylococcus aureus DNA sequence encoding three ORFs, complete cds; prophage phi-11 sequence homology, 5' flank	66	260	906
+ — — - ! !	 	1098	2870	gb L19300 gb L19300	Staphylococcus aureus DNA sequence encoding three ORFs, complete cds; prophage phi-11 sequence homology, 5' flank	<u>ი</u>	866	1773
 	• + • • •	·	434	gb U31979 fb U31979	Staphylococcus aureus chorismate synthase (aroC) and nucleoside diphosphate kinase (ndk) genes, complete cds, dehydroauinate synthase (aroB) and geranylgeranyl pyrophosphate synthetase homolog (gerCC) genes, partial cds	66	432	432
+ · ! !	·	1211	2395	gb U31979	Staphylococcus aureus chorismate synthase (aroC) and nucleoside diphosphate kinase (ndk) genes, complete cds, dehydroauinate synthase (aroB) and geranylgeranyl pyrophosphate synthetase homolog (gerCC) genes, partial cds	91	1185	1185
+ 1 1		2409	2801	gb U31979 	Staphylococcus aureus chorismate synthase (aroC) and nucleoside diphosphate kinase (ndk) genes, complete cds, dehydroauinate synthase (aroB) and geranylgeranyl pyrophosphate synthetase homolog (gerCC) genes, partial cds	80	181	393
+ · ! !	 4 	2690	3484	gb L05004	Staphylococcus aureus dehydroquinate synthase (aroB) gene, 3' end cds; 3- phosphoshikimate-1-carboxyvinyltransferase (aroA) gene, complete cds; ORF3, complete cds	100	75	795
+ ! !		3482	4792	gb L05004	Staphylococcus aureus dehydroquinate synthase (aroB) gene, 3' end cds; 3- phosphoshikimate-1-carboxyvinyltransferase (aroA) gene, complete cds; ORF3, complete cds	66	905	1311
	9	4790	5380	gb L05004	Staphylococcus aureus dehydroquinate synthase (aroB) gene, 3' end cds; 3- phosphoshikimate-1-carboxyvinyltransferase (aroA) gene, complete cds; ORF3, complete cds	100	196	591
+ - -	 		l m	emb X76490 SAGL	(S.aureus (bb270) glnA and glnR genes	1 66	336	336
+ — -	2	336	527	emb X76490 SAGL	S.aureus (bb270) glnA and glnR genes	100	189	192
		727	365	gb U73374 	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8K, cap8E, cap8K, cap8E, cap8K,	1000	ئ 4	363
• — — — -	2	2175	1252	gb U73374	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	66	918	924
-	e	1574	1374	gb U73374 	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8K,	96	122	201
 	2	1019	1 705	gb U21221	Staphylococcus aureus hyaluronate lyase (hysA) gene, complete cds	66	306	315
-	- + E		2	emb Z18852 SACF	S.aureus gene for clumping factor	1 86	2588	2814
_	1 -	3881	1953	dbj D28879 STAP	Staphylococcus aureus gene for penicillin-binding protein 1, complete cds	1 66	1873	1929
+	• • • • • • • • • • • • • • • • • • • •	r 			₩}••••••••••••••••••••••••••••••••••••	+		+11111111

Table 1

S. aureus - Coding regions containing known sequences

ORF nt length	744	813	639	1254	1032	6666	213	1899	549	1957	840	969	453	4		L 1	591	564	525	300
HSP nt length	338	495	639	225	838	066	194	489	549	795	478	456	369		653		534	564	195	280
percent	866	100	66	100	66	66	86	82	66	66	66	84	100	100	66	100	86	96	100	97
match gene name	Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB, dltC and dltD genes, complete cds	S.aureus (bb270) glnA and glnR genes	Staphylococcus aureus lac repressor (lacR) gene, complete cds and lacA repressor (lacA), partial cds	Staphylococcus aureus helicase required for T181 replication (pcrA) gene, complete cds	Staphylococcus aureus helicase required for T181 replication (pcrA) gene, complete cds	(S.aureus factor essential for expression of methicillin resistance (femA) gene, complete cds, and trpA gene, 3' end	S.aureus factor essential for expression of methicillin resistance (femA) gene, complete cds, and trpA gene, 3' end	S.aureus gene for clumping factor	S.aureus (RN4220) genes for potential ABC transporter and potential	S.aureus (RN4220) genes for potential ABC transporter and potential membrane spanning protein	Staphylococcus aureus DNA sequence encoding three ORFs, complete cds; prophage phi-11 sequence homology, 5' flank	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	Staphylococcus aureus hlb gene for beta-hemolysin	Staphylococcus aureus hlb gene for beta-hemolysin		(O)	Staphylococcus aureus type-I signal peptidase SpsA (spsA) gene, and type-I signal peptidase SpsB (spsB) gene, complete cds	Staphylococcus aureus type-I signal peptidase SpsA (spsA) gene, and type-I signal peptidase SpsB (spsB) gene, complete cds	S.aureus sigma factor (plaC) gene, complete cds	S.aureus sigma factor (plaC) gene, complete cds
match acession	dbj D86240 D862 dbj D86240 D862	emb X76490 SAGL	gb M32103	gb M63176 	gb M63176	emb X17688 SAFE	emb X17688 SAFE	emb 218852 SACF	emb 230588 SAST	 emb 230588 SAST 	gb L19300 	gb L14017	emb X13404 SAHL	emb X13404 SAHL	emb X13404 SAHL	dp M63177	dp 10650001	gb U65000 gb U65000	gb M63177	gb M63177
Stop (nt)	1 745	+ 816 	₩	1 1255	1 2284	1001	1195	1 3228	51	1323		1105 1105 	4-6-6-6-6-6-6-6-6-6-6-6-6-6-6-6-6-6-6-6	475	l CO	1 480	592	+ 1153 	1 0	1 784
Start (nt)	2	1 (2)		l N	3315	1999	1407	5126	l M	529	I OS	Ιœ	. 0		746			1716	l W	1 485
9 ORF	 	·	 	·	~ ~ ·	·	2	2 -		5		2		2 -	 	i 	 	2	 	5
1 E H	. —	609	614	1 (2)		629	629	+ 631	632	1 632	+ 651 	i iΩ	1 662	1 662	1 662	682	685	685	0	1 697

Table 1

S. aureus - Coding regions containing known sequences

nt jth	489	180	540	636	369		നി	555	615	363	231	465	174	159	396	285	273	195	165	264	159	1212
ORF nt length		- -	 	 	 					- - -	 		-	 	 	 	 	 	- -	-		
HSP len	217	140	522	618	340	567	429	550	568	363	196	156	174	131	395	131	265	195	163	247	147	1212
percent	66	76	81	66	66		66	98	6 6	86	96	<u>ი</u>	66	100	6	66	86	100	6 6	66	95	66
match gene name	Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB,	Staphylococcus aureus norAl199 gene (which mediates active efflux of fluoroquinolones), complete cds	Staphylococcus aureus DNA for LukM component, LukF-PV like component, complete cds	Staphylococcus aureus V8 serine protease gene	Staphylococcus aureus V8 serine protease gene	Staphylococcus aureus (Wood 46) gene for alpha-toxin	S.aureus partial sod gene for superoxide dismutase	phylococcus aureus MHC class II analog gen	Staphylococcus aureus novel antigen gene, complete cds	Staphylococcus aureus HSP10 and HSP60 genes	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	recf cluster: dnaA=replisome assembly proteingyrB=DNA gyrase beta subunit [Staphylococcus aureus, YB886, Genomic, 5 genes, 3573 nt]	Staphylococcus aureus gyrase-like protein alpha and beta subunit (grlA and grlB) genes, complete cds	Staphylococcus aureus gyrase-like protein alpha and beta subunit (grlA and grlB) genes, complete cds	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	S. aureus norA gene	S.aureus agrA, agrB and hld genes	S.aureus agrA, agrB and hld genes	S.aureus (RN4220) genes for potential ABC transporter and potential membrane spanning protein	S.aureus tagatose 6-phosphate isomerase gene, complete cds	S.aureus tagatose 6-phosphate isomerase gene, complete cds	S.aureus ptsH and ptsI genes
+	dbj D86240 D862	gb M80252	 dbj D83951 STAL 	lemb Y00356 SASP	 emb x00356 SASP	emb X01645 SATO	emb 249245 SA42	gb U20503	dp n63529	dbj D14711 STAH	emb X58434 SAPD	db s77055	gb L25288	gb L25288	 emb X64172 SARP 	dbj D90119 STAN	emb x52543 sAAG	emb X52543 SAAG	emb 230588 SAST	gb M64724	gb M64724	temb X93205 SAPT
Stop (nt)	503	205	1197			0	1 950	5		l 🕁	302	1 467	175	318		ΙCO	ו הט	1 522	ια			1215
Start (nt)	1 15	1 26	1 1736	 - - - - - - - -	t co	1308				ıœ			1 348	ı	792	 - - - - -		1 716	+ 517 		l m	1 2426
ORF	 	; 	 	- - - - -	-+	; 	 	 	 	 	 	; 	i 	; 2 	i 	 	+ -			+		i
Contig	710	1 733	1 47	lΩ	ı ک	756	l	iòo	1 784		798	1 0	848 	I 44		883	ıσο	Ιœ	912		917	

Table 1

S. aureus - Coding regions containing known sequences

Contig	++ ORF ID	Start (nt)		-+	match gene name		HSP nt length	ORF nt length
1 967	+ -		+ 411 	dbj D90119 STAN	S. aureus norA gene			
		672	1 337	emb X52543 SAAG	S.aureus agrA, agrB and hld genes		336	336
	1	ı — i	845		Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	78	190	
1001		498	265	dbj D86240 D862	Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB,	66	234	234
1010	1 -	ri	1 285		gene, c		224	285
		656	i m i	emb X72700 SAPV	S.aureus genes for S and F components of Panton-Valentine leucocidins		205	
9 1		480	· α		decarboxylas		1 00	195
1073		1176	1 589	1gb1K029851	aureus (strain RN450) transposon Tn554 insert	100	131	588
0 1	·	က	230	dbj D86240 D862	- -	66	228	228
	2	218	484	dbj D86240 D862	Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB, dltC and dltD genes, complete cds	100	267	267
o i	m	460	645	dbj D86240 D862	Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB, dltC and dltD genes, complete cds	100	186	186
	i	289	146	lemb X58434 SAPD	ureus p	86	124	144
1143	-	F-1	1 243	gb M63177		66	243	243
1157	 	2		emb 248003 SADN	S.aureus gene for DNA polymerase III			
	1 1	720	1 361	b S74031	norA=NorA {ISP794} {Staphylococcus aureus, NCTC 8325, Insertion, 1820 nt}	66	360	360
- •	i	2	1 283	gb M21854	gulator protein, c	100	282	282
H i	5 -	1127	888	emb X52543 SAAG	S.aureus agrA, agrB and hld genes	100	240	240
- 2		2	9 1	mb X17679 SACO	Staphylococcus aureus coa gene for coagulase	97		
	-	2	529	dbj D86240 D862	Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB, dltC and dltD genes, complete cds	66	495	528
_	-	- 1 	1 210	gb S74031)	norA=NorA (ISP794) (Staphylococcus aureus, NCTC 8325, Insertion, 1820 nt)	100	210	210
1301		41	472	emb X76490 SAGL	S.aureus (bb270) glnA and glnR genes	66	299	432
	•		-	-		•	•	•

Table 1

S. aureus - Coding regions containing known sequences

	-	(111.5)	l acession		ident	length	length
9 1 1 -	 	326	emb X64172 SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta 6 beta' chains	80	277	300
	2	175		ccus aureus gene for	86	139	174
 	346	675	dbj D86240 D862	d dlt operon dlt.	86	672	672
97 1 6	44	324	gb U73374	phylococcus aureus type 8 capsule genes, p8E, cap8F, cap8G, cap8H, cap8I, cap8J, c	66	321	321
1857 1 1	- - - - - - -	192	gb M90536	ylococ	86	192	192
23 1 1 +	· 0	181	emb X17688 SAFE	aureus factor essential for expression of met gene, complete cds, and trpA gene, 3' end	100	180	180
957 1 2		346	ab U605891	ylococcus aureus novel antigen gene,	1 66 1	345	345
		402	dbj D86240 D862	Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB, dltC and dltD genes, complete cds	100 -	402	
00 1 4	-	208	gb M63177	S.aureus sigma factor (plaC) gene, complete cds	1 66	207	207
		402	ı —	taphylococcus aureus DNA frag	1 66 1	131	
537 1 30	308	156	emb X17688 SAFE	aureus factor essential for expression of metlene, complete cds, and trpA gene, 3' end	66	153	153
91 1	·	400	gb L25426	2 (pbp2) gene, com	1 66 1	399	399
950 1 77	778	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	dbj D30690 STAN	Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete cds	100	358	381
1		398	gb U51132	Staphylococcus aureus o-succinylbenzoic acid CoA ligase (mene), and o-	97	272	396
978 1 61	618	328	gb U31979	synthase (aroC) and a dehydroauinate sonthetase homolog (g	86	250	291
985 1 83	832	464	Х Сип	Staphylococcus aureus coa gene for coagulase	1 86 1	347	369
 	170	1784	gb U11779	aphylococcus aureus methicillin-re RNA spacer region	87	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	387
 	74	238	dbj D30690 STAN	Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete cds	88	178	237
008 2 45	51	281	dbj D30690 STAN	Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete cds	97	120	171

Table 1

S. aureus - Coding regions containing known sequences

ORF nt	368	234	153	6	147	258	213	261	258	, O I	237		153	171	231	174	210	378	210	141
HSP nt	72	234	100	135	135	183	213	234	229	250	215	9	142	88	192	154	197	91	72	141
	66	76	87	100 1	97	77	66	86	66	96	95		6	100	1 86	96	68	96	86	96
match gene name	S.aureus fnbB gene for fibronectin binding protein B	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta- galactosidase (lacG) genes, complete cds	putP) gene, c	oxykinase (pck	Staphylococcus aureus phosphoenolpyruvate carboxykinase (pcka) gene, complete cds	Staphylococcus aureus phosphoenolpyruvate carboxykinase (pcka) gene, complete cds	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete cds	Staphylococcus aureus proline permease homolog (putP) gene, complete cds	s for ribo cted RNA p	Staphylococcus aureus DNA for DNA polymerase III, complete cds	S.aureus gene for DNA polymerase III	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta- galactosidase (lacG) genes, complete cds	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	S.aureus DNA for rpoC gene	S.aureus gene for clumping factor	Staphylococcus aureus genes for DNA gyrase A and B, complete cds		and	Staphylococcus aureus peptidoglycan hydrolase gene, complete cds
match acession	emb x62992 safn	gb J03479	gb U06451	gb U51133 	gb U51133	gb U51133	emb X64172 SARP	dbj D30690 STAN	gb U06451	emb X64172 SARP	dbj D86727 D867	emb 248003 SADN	gb J03479	emb X58434 SAPD	emb X89233 SARP	emb Z18852 SACF	dbj D10489 STAG	emb X58434 SAPD	gb J03479 	gb M76714
l th t		1 235	I M			327		1 261	Ιœ		l m		5	l O	l es	1 [-	211 211	, <u>r</u>	211	143
Start (nt)	793	2	81	06	18	70	i i i i m	 	27	2	1 1 1 1 1 1 1 1 1	444	307	268	1 463		1 420		1 420	
ORF					· · · · · · · · · · · · · · · · ·	2			· - ·		i 			 			+ - ·	 +4 	 ~ 	
ΙËΗ			02	iò	03	03	10	10	3073	3074	3088	3097	10	12	12	I —	1 3160	17		3210

Table 1

S. aureus - Coding regions containing known sequences

†			+ · 	† — ₁	t — -	 	+	+ — ·	+ 				+ -	 		†	+ -	+ — ·		⊦ — + I		
+	ORF nt length	825	393	243	318	180	219	1 38 1 1 38 1 1	165	420		348	378	393		234	192	336	1 240	462	360	402
	HSP nt length	257		102		141	174	7.9	162	175	253	345	346	319	403	231	112	229	81	367	333	387
+	percent ident	71	66	66	66	1001	86	100	86	86	66	66	72	1 86	84	100	100	100	96	71	85	86
	match gene name	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	S.aureus DNA for rpoC gene	Staphylococcus aureus transfer RNA sequence with two rRNAs	S.aureus gene for clumping factor	Staphylococcus aureus coa gene for coagulase	Staphylococcus aureus coa gene for coagulase	Staphylococcus aureus prolipoprotein diacylglyceryl transferase (lgt) gene,	Staphylococcus aureus prolipoprotein diacylglyceryl transferase (lgt) gene, complete cds	Staphylococcus aureus gene for staphylocoagulase	Transposon Tn5404 and insertion sequences IS1181 and IS1182 (from Staphylococcus aureus) DNA	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta- galactosidase (lacG) genes, complete cds	S.aureus gene for clumping factor	S.aureus gene for clumping factor	S.aureus gene for clumping factor	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for rib L7/L12, hypothetical protein ORF202, DNA-directed RNA beta' chains	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	Saureus find gene for fibronectin binding protein B	Staphylococcus aureus transfer RNA sequence with two rRNAs	S.aureus gene for clumping factor	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains
	match acession	gb L14017	emb X89233 SARP	gb L11530	emb Z18852 SACF	b X17679 SA	emb X17679 SACO	gb U35773	gb U357731 	emb X16457 SAST	gb L43098	gb J03479	emb 218852 SACF	emb 218852 SACF	emb 218852 SACF	emb X64172 SARP	emb X64172 SARP	emb X62992 SAFN	gb L11530	emb 218852 SACF	gb L14017	emb X64172 SARP
	Stop (nt)		ெ க	634	C) I	$ \infty $	I +-1	4 7	9 1	422	9 1			396	1 03 1		415	2		1 463	5	402
	Start (nt)	10	1 0	392	ന	(m)		1 1- 1	527	3	2	(m)	ו כט ו	788	0	l m	1 6 1		ı 60 ا		608	
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	nt ID	23	53	3543	55	55	55	26	56	3566	53	59	09	3602	65	89	89	69	70	3725	76	3767
+		+	· — +	⊦ — ∔	4	+ +	- →	⊦ — -	-	-	 1	-	·	+ +	+ +	·	·	+ - -	⊦ — -	⊦ – ⊣		- +

Table 1

417 396 465 324 285 237 183 177 483 213 249 219 252 171 192 228 381 399 477 177 ORF nt length 155 HSP nt length 170 79 450 159 88 356 209 411 204 123 249 396 161 204 192 347 299 217 171 percent| ident 99 85 96 86 100 98 100 100 100 95 99 98 66 94 16 100 100 97 99 97 87 4 4 ᄲ Ų cds cds; cds; |S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein | L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta | beta' chains (S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein | L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta and phospho-beta |S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, | dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase cds; insferase and dihydrolipoamide dehydrogenase cillin-resistance protein (mecR) gene and complete gene, 3' end ene, complete Staphylococcus aureus dehydroquinate synthase (aroB) gene, 3' end phosphoshikimate-1-carboxyvinyltransferase (aroA) gene, complete complete cds Staphylococcus aureus peptidoglycan hydrolase gene, complete cds complete cds complete cds complete cds complete cds 1S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dene yvinyltransferase (aroA) gene, |S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), | galactosidase (lacG) genes, complete cds synthase (aroB) |Staphylococcus aureus elastin binding protein (ebpS) and B, |Staphylococcus aureus genes for DNA gyrase A and B, В, S.aureus fibronectin-binding protein (fnbA) mRNA, ig protein (fnbA) mRNA, and staphylocoagulase for DNA gyrase A for DNA gyrase A coagulase Staphylococcus aureus dehydroquinate ene for factor for |dbj|D10489|STAG |Staphylococcus aureus genes |Staphylococcus aureus genes |Staphylococcus aureus methi S.aureus fibronectin-bindin dihydrolipoamide acetyltra phosphoshikimate-1-carboxy ORF3, complete cds phosphoshikimate-1-carbox ORF3, complete cds for 23S rRNA complete cds |emb|X16457|SAST |Staphylococcus aureus gene |S.aureus DNA for rpoC gene emb|X89233|SARP |S.aureus DNA for rpoC gene |S.aureus gene for clumping |Staphylococcus aureus coa match gene name gene unknown ORF, beta' chains |S.aureus emb|X17679|SACO emb|X58434|SAPD emb|X89233|SARP emb|X64172|SARP |dbj|D10489|STAG emb|X58434|SAPD |emb|Z18852|SACF emb|X64172|SARP | dbj | D10489 | STAG emb|X68425|SA23 acession gb | M76714 | |gb|J03479| |gb|L14017| gb|J04151| | ap | U48826| gb | L05004 |gb|L05004 match gb|J04151 Stop (nt) 420 400 485 239 286 229 366 398 402 468 400 573 327 253 288 237 173 183 357 251 381 Start (nt) 1049 188 836 48 456 798 650 572 181 542 793 184 932 സ 7 \dashv ന -7 ന ~ ORF ID \sim 7 $\boldsymbol{\dashv}$ ~ \leftarrow 7 -_ \leftarrow \vdash Н $^{\circ}$ ~ ↤ --- 7 -Н Ч Contig 3895 3905 3905 3844 3876 3878 3888 3893 3894 3775 3786 3786 3813 3819 3845 3856 3859 3877 3893 3871 3798 ID

sednences

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Coding regions containing know

S. aureus

Table 1

S. aureus - Coding regions containing known sequences

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ORF nt length	357	33(348	192	9	348	375		303	345	300	276		381	162	213	9	357	294
HSP nt length	278	175	295		339		271	429	198	127	227	276	307	157	8 8	200		297	240
percent ident	66	75	100	86	66	8 7	96	66	75	86		66	74	86	100	66	87	66	86
	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	S.aureus gene for DNA polymerase III	Staphylococcus aureus gene for staphylocoagulase	Staphylococcus aureus genes for DNA gyrase A and B, complete cds	S.aureus gene for clumping factor	S.aureus gene for clumping factor	S.aureus gene for DNA polymerase III	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	Ď	Transposon Tn5404 and insertion sequences IS1181 and IS1182 (from Staphylococcus aureus) DNA	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	S.aureus gene for clumping factor	Staphylococcus aureus dehydroquinate synthase (aroB) gene, 3' end cds; 3- phosphoshikimate-1-carboxyvinyltransferase (aroA) gene, complete cds; ORF3, complete cds	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	S.aureus fibronectin-binding protein (fnbA) mRNA, complete cds	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains
match acession	emb X58434 SAPD	gb L14017	emb 248003 SADN	emb X16457 SAST	dbj D10489 STAG	emb 218852 SACF	emb 218852 SACF	emb 248003 SADN	gb L14017	gb U11786 	gb L43098	emb X58434 SAPD	emb 218852 SACF	db L05004	gb U73374 	gb J04151	gb L14017	emb X64172 SARP	emb X64172 SARP
1 47 4	359	330	347	390	371	1 4T	375	432	304	402	301	772	10	402	401	247	366		294
Start (nt)	e		I O	199	F (C)	692				58	7	2		22	240	35	1 0	754	
ORF			 			+ — - H				 	+ — — · ! ! !								
ıщн	I ON I	91	3964	00	03	i 0	90	90		4085	4088	4093	60		4125	i i	15	4154	4179
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Table 1

S. aureus - Coding regions containing known sequences

ΙĢΗ	ORF I	Start (nt)	Stop (nt)	match acession	 match gene name	percent ident	HSP nt length	++ ORF nt length
	+		5	emb X89233 SARP	S.aureus DNA for rpoC gene	66	239	255
20			1 303	emb 218852 SACF	S.aureus gene for clumping factor			
20	2	195	4	emb 218852 SACF	S.aureus gene for clumping factor	95	65	150
	 	108		emb X58434 SAPD		68	76	207
4216	; — — · ! ! — — ·	656		emb X58434 SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	8 6	326	327
22			- 298	gb L11530		1 6	132	1 297 1
1 40	; — — · 		ι σο	gb U11784	Staphylococcus aureus methicillin-resistant ATCC 33952 clone RRNV40 16S-23S rRNA spacer region	80	141	168
27	 	355	+ 179	emb 248003 SADN	S.aureus gene for DNA polymerase III	100	164	177
				emb(X16457 SAST	Staphylococcus aureus gene for staphylocoagulase	66	150	174
4277		£1	I ~	lemb X64172 SARP	nd rpoc gene 02, DNA-dire	66		270
4282		691	377	emb x64172 SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	86	282	315
4291		379	<u>)</u> ග	emb x64172 SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	66	183	189
1 4295		3	329	emb X16457 SAST	Staphylococcus aureus gene for staphylocoagulase	94	144	327
31		435	l co	gb L11530	nsfer RNA sequence wi	100	94	
ı —	 -	8	185	gb J03479	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta- galactosidase (lacG) genes, complete cds	100	158	183
4315	2	101	-	gb J03479	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-	86	75	210
4327			1 294	gb L43098	Transposon Tn5404 and insertion sequences IS1181 and IS1182 (from Staphylococcus aureus) DNA	86	294	294
1 4360		603	1 319	gb U02910	aphylococcus aureus ATCC 25923 16S rRNA gene, partial	100	116	285
9		e	4	emb X64172 SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	95	140	144
4388	 	167	310	emb X62992 SAFN	S.aureus fnbB gene for fibronectin binding protein B	73	119	144
)				•	·	

Table 1

S. aureus - Coding regions containing known sequences

Contig	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
40	 		313	emb X62992 SAFN	S.aureus fnbB gene for fibronectin binding protein B	1 6 1	243	312
1 0 1	 - 	36	1 00 1	dbj D12572 STA2	Staphylococcus aureus rrnA gene for 23S ribosomal RNA			246
4	 -		ெரை	emb 218852 SACF	S.aureus gene for clumping factor	85	185	291
1 4428		403	1 5	emb X64172 SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	100	139	246
4462	• • • — — — •	8	271	emb X64172 SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	თ თ	270	270
	 	-	1 240	emb 218852 SACF	S.aureus gene for clumping factor	66 1	231	240
4469	 	 	. ⊢	gb J03479	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta- galactosidase (lacG) genes, complete cds	66	265	312
4485		ო — — -	9	gb L43098	Transposon Tn5404 and insertion sequences IS1181 and IS1182 (from Staphylococcus aureus) DNA	86	259	261
4492	! ! !	74	400	gb M86227	Staphylococcus aureus DNA gyrase B subunit (gyrB) RecF homologue (recF) and DNA gyrase A subunit (gyrA) gene, complete cds	85	104	327
4	• - - - - - -	- 535		emb Z18852 SACF	S.aureus gene for clumping factor	66	213	267
4529	 	2	172	emb X64172 SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	100	151	171
54	 		0	emb x62992 SAFN	S.aureus fnbB gene for fibronectin binding protein B	100	157	300
4554	 	318	160	emb 218852 SACF	S.aureus gene for clumping factor	84	126	159
56		6		emb 218852 SACF	S.aureus gene for clumping factor	84	⊢ 1	219
1 4569		1 79	1 0 1	emb Z18852 SACF	S.aureus gene for clumping factor	86	127	144
		2	-	lemb X58434 SAPD	IS.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	92	168	195
4614	 	1 464		emb 218852 SACF	S.aureus gene for clumping factor	98	169	231
		105	302	gb J04151	S.aureus fibronectin-binding protein (fnbA) mRNA, complete cds	66	152	198
4632		-	0	gb J03479 	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta- galactosidase (lacG) genes, complete cds	86	183	189
64			2 (emb 218852 SACF	S.aureus gene for clumping factor	8 4	100	222
1 4687	-	5	166	gb J04151	S.aureus fibronectin-binding protein (fnbA) mRNA, complete cds	86	156	165
) 							.

S. aureus - Coding regions containing known sequences

Contig ID	Contig ORF ID	Start (nt)	Stop (nt)	match acession	I match gene name	percent HSP nt ident length	— - ·	ORF nt length
4695	+	+	158	gb L14017 	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	75	155	156
4703	+ +	 - - - - - -	+ 153 	emb X58434 SAPD	emb X58434 SAPD S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	 86	103	153